Amendments to the Specification:

Please delete the current sequence listing and insert the substitute sequence listing after the Abstract.

Please replace the paragraph at page 19, line 37 with the following:

According to preferred aspects of the present invention the compound is a cyclic peptide or analog thereof. Preferably, the compound has the following formula:

X_i-Cys_1-X_j-Cys_2-X_k (SEQ ID NO: 101)

wherein X_i is absent or is a peptide of between 1 and 100 amino acids, preferably between about 1 and 50 amino acids, and more preferably between about 1 and 10; X_j is 5 amino acids and X_k is absent or a peptide of between 1 and 100 amino acids, preferably between about 1 and 50 amino acids and more preferably between about 1 and 10, so long as the cyclic peptide or analog thereof retains the qualitative biological activity described above.

Please replace the paragraph at page 21, line 5 with the following:

Preferred peptides of the present invention have the following formula:

X_i-Cys_1-X_j-Cys_2-X_k (SEQ ID NO: 101)

wherein X_i is absent or is between 1 and 100 amino acids; X_j is 5 amino acids and X_k is absent or between 1 and 100 amino acids. Preferably, X_i and X_k are between 1 and 50 amino acids and more preferably between 1 and 10 amino acids.

Please replace the paragraph at page 21, line 10 with the following:

By way of exemplification and not limitation, ~~prefered~~ preferred peptides of the present invention include the peptides described in Figure 4. In general, a preferred peptide has the formula:

X_i-Cys_1-X_j-Cys_2-X_k (SEQ ID NO: 109)

wherein;

X_j has the formula

-Xaa_8-Xaa_9-Xaa_{10}-Xaa_{11}-Xaa_{12}-

and Xaa_8 is an amino acid selected from the group ~~consising~~ consisting of Trp, Thr, Ala, Phe, Leu, Met and Tyr; Xaa_9 is an amino acid selected from the group consisting of Thr, Asp and Ala;

Xaa_{10} is an amino acid selected from the group consisting of Trp, Ala, Phe, Leu and Tyr; Xaa_{11} is an amino acid selected from the group consisting of Glu, Ala, Arg and Gln; and Xaa_{12} is an amino acid selected from the group consisting of Gly, Asp, Thr, Ser and Ala.

Please replace the paragraph at page 21, lines 23 with the following:

As a further example, preferred peptides have the formula:

Xaa_1- Xaa_2- Xaa_3- Xaa_4- Xaa_5- Xaa_6-Cys- Xaa_8- Xaa_9- Xaa_{10}- Xaa[[1]]$_{11}$- Xaa[[1]]$_{12}$-Cys- Xaa_{14}- Xaa_{15}- Xaa_{16}- Xaa_{17}- Xaa_{18} (SEQ ID NO: 102)

wherein Xaa_1 is any amino acid; Xaa_2 is any amino acid; Xaa_3 is an amino acid selected from the group consisting of Trp, Phe, Leu, Ala, Met and Val; Xaa_4 is an amino acid; Xaa_5 is an amino acid selected from the group consisting of Val, Ile, Ala, Trp and Tyr; Xaa_6 is an amino acid selected from the group consisting of Leu, Ile, Met, Val and Ala; Xaa_8 is selected from the group consisting of Trp, Phe, Leu, Met, Ala and Val; Xaa_9 is an amino acid ; Xaa_{10} is an amino acid selected from the group consisting of Trp, Phe, Met and Tyr; Xaa_{11} is any amino acid; Xaa_{12} is any amino acid; Xaa_{14} is any amino acid except Pro; Xaa_{15} is an amino acid selected from the group consisting of Arg, Lys, Leu, Trp, His and Met;

Xaa_{16} is any amino acid; Xaa_{17} is any amino acid; and Xaa_{18} is any amino acid.

Please replace the paragraph at page 40, line 38 with the following:

Phage Libraries - The random sequence polyvalent peptide phage libraries have been described previously (Lowman, H. B., *et al.*, *Biochemistry* 37:8870 (1998)). The peptide libraries were of the form $X_iCX_jCX_k$ (SEQ ID NO:103) (where X was any of the 20 naturally ocurring L-amino acids and j ranged from 4-10 and i + j + k=18), an unconstrained library X_{20} (SEQ ID NO:104), and $X_4CX_2GPX_4CX_4$ (SEQ ID NO:105). Each of the 10 libraries has in excess of 10^8 clones.

Please replace the paragraph at page 41, line 1 with the following:

Selection Conditions - TF_{1-243} (Paborsky, L. R., *et al.*, J. Biol. Chem. 266: 21911 (1991)) or recombinant human FVIIa (2 μg/ml each) were immobilized directly to ~~Maxisorp~~ MaxiSorp™ plates (Nunc) in 50 mM ammonium bicarbonate, pH 9.3 by incubating overnight at 4 °C. Wells were blocked using Sorting Buffer (50 mM HEPES, pH 7.2, 5 mM $CaCl_2$, 5 mM $MgCl_2$, 150 mM NaCl, 1% BSA) for 1 h at 25 °C. Recombinant human FVIIa (2 μg/ml) in Sorting Buffer

was added for 30 min to wells previously coated and blocked with TF to form the TF-FVIIa complex. Phage from the libraries described above were pooled into 3 groups. Pool A contained $X_iCX_jCX_k$ (SEQ ID NO:103) where j = 5 - 7; Pool B contained $X_4CX_2GPX_4CX_4$ (SEQ ID NO:105), X_{20} (SEQ ID NO:104) and $X_iCX_jCX_k$ (SEQ ID NO:103) where j = 4; Pool E contained $X_iCX_jCX_k$ (SEQ ID NO:103) where j = 8 - 10. Phage from each pool were incubated with the immobilized targets in Sorting Buffer for 3 h at 25 °C.; generally about 5 x 10^{10} phage were added at the beginning of each round. Unbound phage were removed by repetitive washing with Wash Buffer (50 mM HEPES, pH 7.2, 150 mM NaCl, 0.005% Tween 20™); remaining phage were eluted with 500 mM KCl, 10 mM HCl, pH 2. The eluted phage were then propagated in XL1-Blue cells with VCSM13 helper phage (Stratagene™) overnight at 37 °C. Enrichment could be monitored by titering the number of phage which bound to a target coated well compare to a well coated with BSA.

Please replace Table II at page 48 with the following:

Table II. Sequences Selected Using Selected Full Randomization of the A Series

SEQUENCE ID. NO.	CLONE	DEDUCED AMINO ACID SEQUENCE
106	Library AoN	o o X W E V X C W X W E X C X X X X X X
76	AN41	A W E V L C W A W E D C E R G A G S
77	AN33	A W E V V C W S W E T C E R G E T P
78	AN31	E W E V V C W A W E T C E R G E R Q
79	AN43	E W E V L C W E W E V C E R D I T L
80	AN42	E W E V V C W T W E A C E L G E R V
81	AN32	G W E V V C W S W E S C A R G D L E
107	Library AoNC	o o X W E V X C W X W E X C X o o o o o
82	ANC45	A W E V V C W S W E T C E
83	ANC41	E W E V V C W E W E N C L
84	ANC33	E W E V L C W G W E T C S
85	ANC34	G W E V L C W T W E E C S

86	ANC43			S	W	E	V	L	C	W	Q	W	E	E	C	E							
87	ANC32			T	W	E	V	L	C	W	S	W	E	S	C	E							
108	Library A	X	X	X	W	E	V	X	C	W	X	W	E	X	C	X	X	X	X	X	X		
88	AP31	M	E	T	W	E	V	L	C	W	E	W	E	E	C	V	R	G	G	E	P		
89	AP32	A	V	E	W	E	V	I	C	W	A	W	E	T	C	E	R	S	N	M	Q		
90	AP33	A	V	Q	W	E	V	L	C	W	Q	W	E	N	C	H	R	G	E	Q	V		
91	AP34	M	Q	G	W	E	V	V	C	W	E	W	E	G	C	A	R	G	D	H	Q		
92	AP42	E	E	Q	W	E	V	V	C	W	D	W	E	T	C	D	W	P	G	K	D		
93	AP43	L	G	E	W	E	V	M	C	W	T	W	E	S	C	G	W	P	V	G	S		
94	AP44	M	L	D	W	E	V	V	C	W	T	W	E	S	C	V	R	E	G	K	Q		
95	AP45	K	N	G	W	E	V	L	C	W	T	W	E	T	C	G	R	G	V	G	D		
96	AP35	G	A	P	W	E	V	V	C	W	S	W	E	S	C	S	W	G	V	A	S		
97	AP41	E	D	L	W	E	V	V	C	W	S	W	E	A	C	S	R	E	G	T	Q		

- Peptide sequences were deduced from the DNA sequence of clones obtained after 4 rounds of selection.
- Shaded residues indicate the wildtype sequence which was fixed; underlined residues were fully randomized as described in text.
- "o" indicates no amino acid.